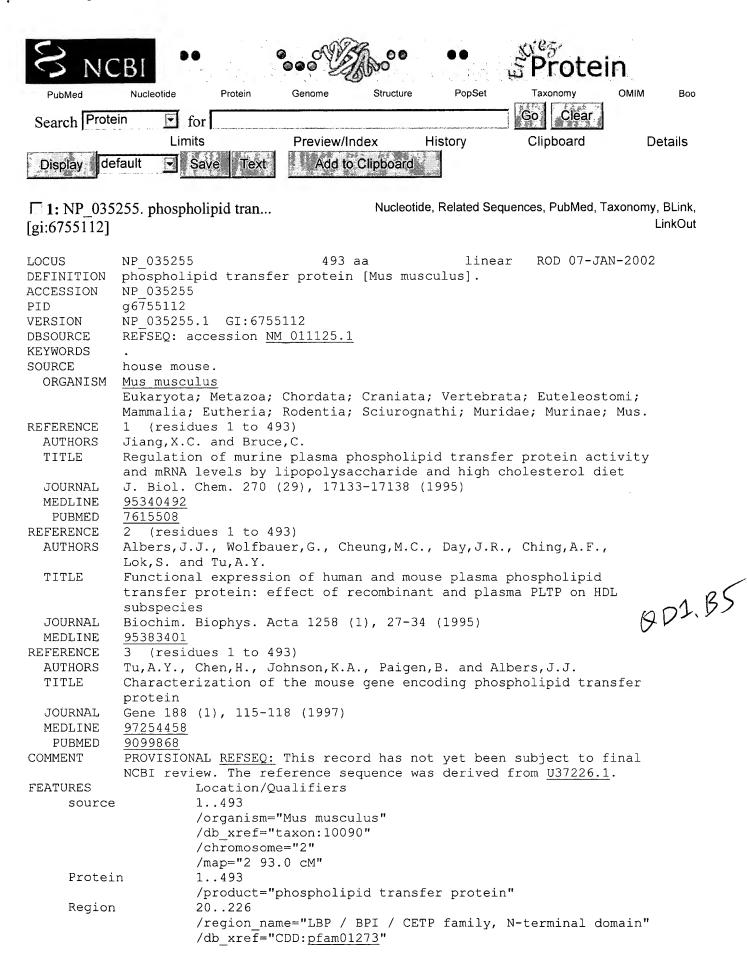


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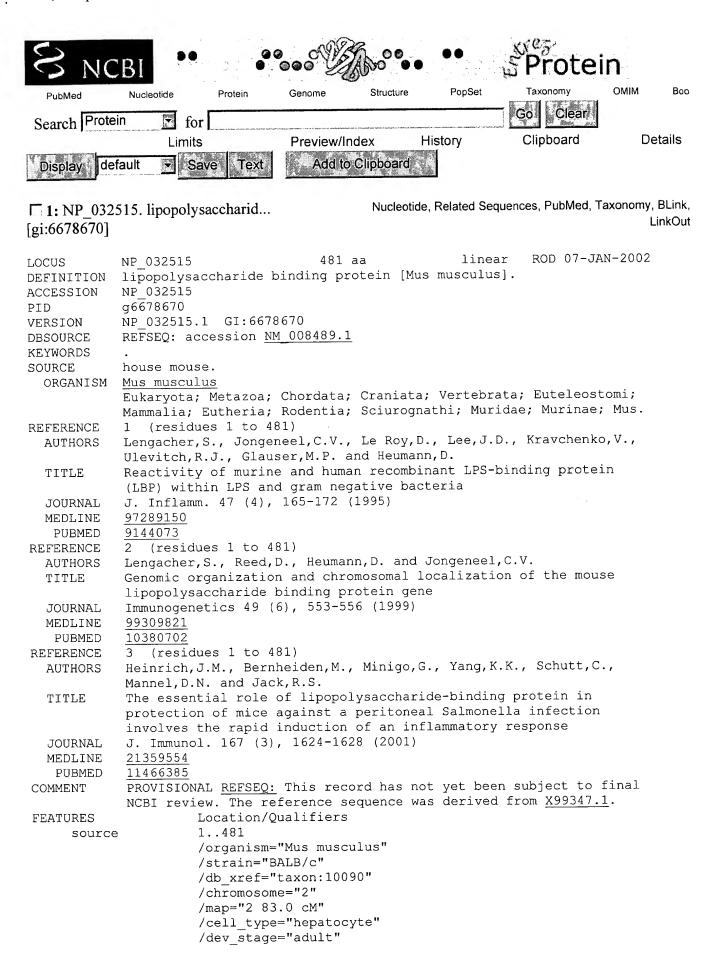
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      121 egvsirtglq lsqdssgrik vsnvsceasv skmnmafggt frrmynffst fitsgmrfll
      181 nqqicpvlyh agtvllnsll dtvpvrssvd dlvgidysll kdpvvsngnl dmefrgaffp
      241 lkednwslpn ravepqledd ermvyvafse fffdsamesy fqagalqltl vgdkvpsdld
      301 mllratyfgs ivllsptvin splklkleat spprctikps gttisitasv titlappmlp
      361 evelskmime grlsakltlr gkalrvkldl rrfqiysnqs aleslalipl qaplktllqi
      421 gvmpllnert wrgvqiplpe ginfvrevvt nhagfvtvga dlhfakglre vidknrpadv
      481 aashvpppsa aaa
11
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                     /note="LBP BPI CETP"
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                     /db xref="CDD:smart00328"
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                     /note="LBP BPI CETP C"
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                     /note="BPI2"
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      121 sflklhqsfd ldvkgvtisv dlllgmdpsg rptvsasgcs sricdldvhi sgnvgwllnl
      181 fhnqiesklq kvlenkvcem iqksvtsdlq pylqtlpvta eidnvlgidy slvaapqaka
      241 qvldvmfkge ifnrnhrspv atptptmslp edskqmvyfa isdhafnias rvyhqagyln
      301 fsitddmlph dsgirlntka frpftpqiyk kypdmklell rtvvsapiln vspqnlslap
      361 qmeiegfvil ptsarepvfr lsvvtnvfas ltfntrkvtg mlhpdkagvr lieskvgifn
      421 vnlfqaflny yllnslypdv naelaqgfpl plprhiqlhd ldfqirkdfl ylganvqymr
      481 v
//
```

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S NCBI	• • • •	••• E	1 000 •	••	్ట్ Protei	n	
PubMed Nucle	otide Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Boo
Search Protein	for				Go Clear		
Limits		Preview/Index History		istory	Clipboard	Details	
Display default	Save Text	Add to	Clipboard				

1: O61805. LIPOPOLYSACCHARID...[gi:2497616] Related Sequences, PubMed, Taxonomy, BLink, LinkOut

481 aa linear ROD 15-JUL-1998 LBP MOUSE LOCUS DEFINITION LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP). ACCESSION 061805 q2497616 PID Q61805 GI:2497616 VERSION swissprot: locus LBP MOUSE, accession Q61805; DBSOURCE class: standard. created: Nov 1, 1997. sequence updated: Nov 1, 1997. annotation updated: Jul 15, 1998. xrefs: gi: gi: 1430866, gi: gi: 1430867 xrefs (non-sequence databases): HSSP P17213, MGD MGI:1098776, PFAM PF01273, PROSITE PS00400 Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal. KEYWORDS SOURCE house mouse. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (residues 1 to 481) REFERENCE Lengacher, S., Jongeneel, C.V., Le Roy, D., Lee, J.D., Kravchenko, V., AUTHORS Ulevitch, R.J., Glauser, M.P. and Heumann, D. Reactivity of murine and human recombinant LPS-binding protein TITLE (LBP) within LPS and gram negative bacteria J. Inflamm. 47 (4), 165-172 (1995) JOURNAL MEDLINE 97289150 9144073 PUBMED SEQUENCE FROM N.A. REMARK STRAIN=BALB/C COMMENT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from http://www.expasy.ch/sprot and http://www.ebi.ac.uk/sprot _____ [FUNCTION] BINDS TO THE LIPID A MOIETY OF BACTERIAL LIPOPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS TO INTERACT WITH THE CD14 RECEPTOR. [SIMILARITY] BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY. FEATURES Location/Qualifiers source 1..481

/organism="Mus musculus" /db xref="taxon:10090"

1..481

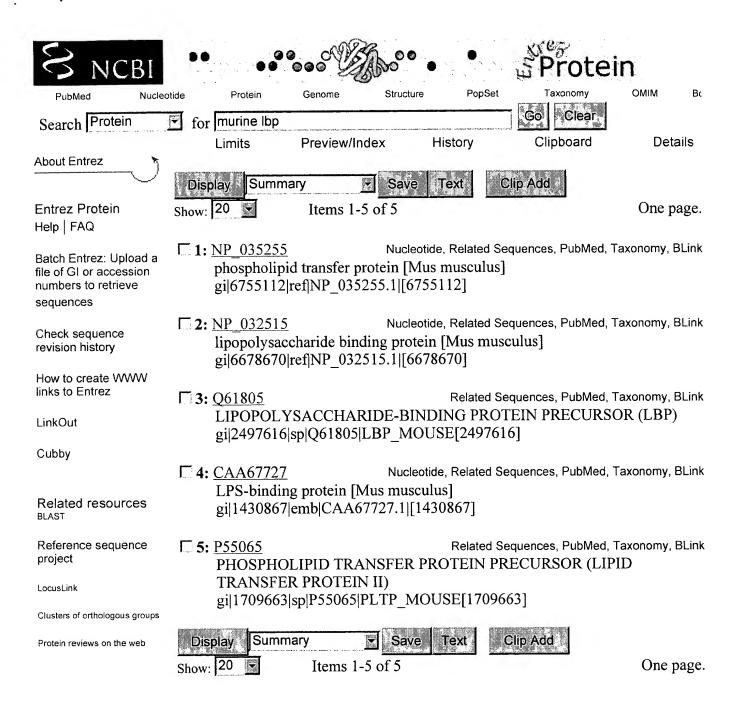
Protein 1..481

/product="LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR"

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                     355
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      121 sflklhgsfd ldvkgvtisv dlllgmdpsg rptvsasgcs sricdldvhi sgnvgwllnl
      181 fhnqiesklq kvlenkvcem iqksvtsdlq pylqtlpvta eidnvlgidy slvaapqaka
      241 qvldvmfkge ifnrnhrspv atptptmslp edskqmvyfa isdhafnias rvyhqagyln
      301 fsitddmlph dsgirlntka frpftpqiyk kypdmklell rtvvsapiln vspgnlslap
      361 qmeiegfvil ptsarepvfr lsvvtnvfas ltfntrkvtg mlhpdkagvr lieskvgifn
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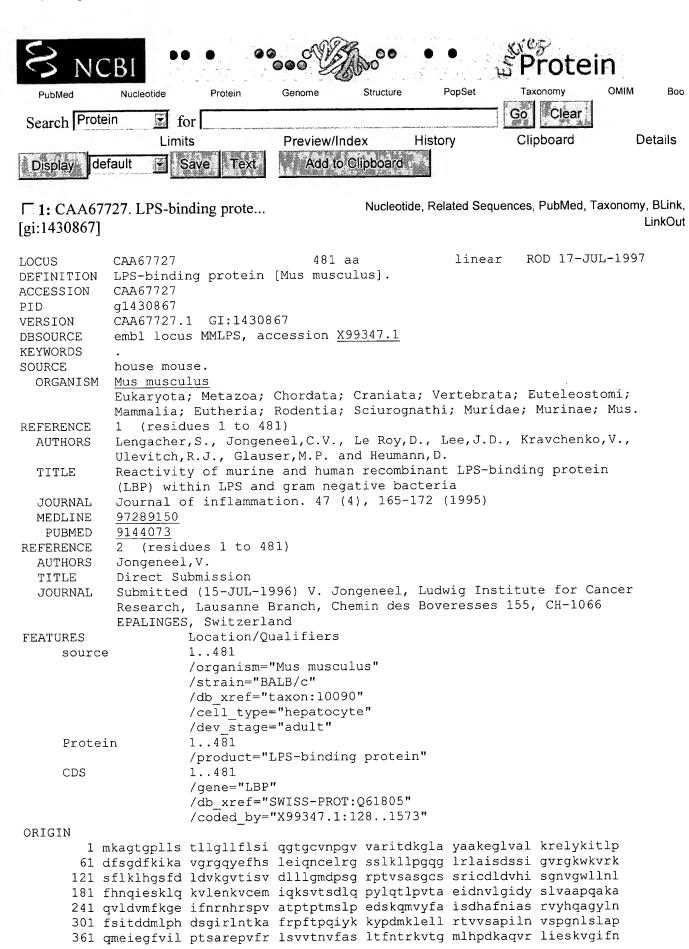
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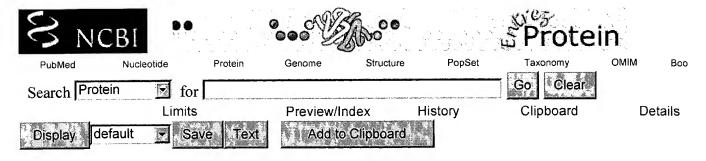
spare-sun-solaris2.8 Mar 25 2002 14:04:41

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1: P55065. PHOSPHOLIPID TRAN...[gi:1709663] Related Sequences, PubMed, Taxonomy, BLink, LinkOut

PLTP MOUSE 493 aa linear ROD 01-NOV-1997 LOCUS PHOSPHOLIPID TRANSFER PROTEIN PRECURSOR (LIPID TRANSFER PROTEIN DEFINITION

II).

ACCESSION P55065 g1709663 PID

VERSION P55065 GI:1709663

swissprot: locus PLTP MOUSE, accession P55065; DBSOURCE

> class: standard. created: Oct 1, 1996.

sequence updated: Oct 1, 1996. annotation updated: Nov 1, 1997.

xrefs: gi: gi: 1051265, gi: gi: 1051266, gi: gi: 902887, gi: gi:

902888

xrefs (non-sequence databases): HSSP P24337, MGD MGI:103151, PFAM

PF01273, PROSITE PS00400

Lipid transport; Glycoprotein; Signal. KEYWORDS

SOURCE house mouse. ORGANISM Mus musculus

> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE (residues 1 to 493)

Albers, J.J., Wolfbauer, G., Cheung, M.C., Day, J.R., Ching, A.F., **AUTHORS**

Lok, S. and Tu, A.Y.

Functional expression of human and mouse plasma phospholipid TITLE transfer protein: effect of recombinant and plasma PLTP on HDL

subspecies

Biochim. Biophys. Acta 1258 (1), 27-34 (1995) **JOURNAL**

MEDLINE 95383401

SEOUENCE FROM N.A. REMARK REFERENCE (residues 1 to 493) Jiang, X.C. and Bruce, C. AUTHORS

TITLE Regulation of murine plasma phospholipid transfer protein activity

and mRNA levels by lipopolysaccharide and high cholesterol diet

J. Biol. Chem. 270 (29), 17133-17138 (1995) **JOURNAL**

MEDLINE 95340492

REMARK SEQUENCE FROM N.A.

STRAIN=C57BL/6

COMMENT

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and http://www.ebi.ac.uk/sprot

[FUNCTION] CONVERTS HDL INTO LARGER AND SMALLER PARTICLES. MAY PLAY A KEY ROLE IN EXTRACELLULAR PHOSPHOLIPID TRANSPORT AND MODULATION

OF HDL PARTICLES.

h

cb

h g

e e

e e fcg

e

e

ge

```
[TISSUE SPECIFICITY] HIGHEST IN LUNG, ADIPOSE TISSUE, BRAIN, AND
            HEART.
            [SIMILARITY] BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
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                      /site_type="glycosylation"
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     Region
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121 egvsirtglq lsqdssgrik vsnvsceasv skmnmafggt frrmynffst fitsgmrfll
181 nqqicpvlyh agtvllnsll dtvpvrssvd dlvgidysll kdpvvsngnl dmefrgaffp
241 lkednwslpn ravepqledd ermvyvafse fffdsamesy fqagalqltl vgdkvpsdld
301 mllratyfgs ivllsptvin splklkleat spprctikps gttisitasv titlappmlp
361 evelskmime grlsakltlr gkalrvkldl rrfqiysngs aleslalipl qaplktllqi
421 gvmpllnert wrgvqiplpe ginfvrevvt nhagfvtvga dlhfakglre vidknrpadv
481 aashvpppsa aaa
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